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<151> 2004.03.05

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Gly Trp Asn Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu	
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Arg Asp Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro	
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Asn Trp Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp	
210 215 220 225	
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His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala	
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Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly Asn	
245 250 255	
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Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe	
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Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro Tyr	
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Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile	
290 295 300 305	
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Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly Ala	
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Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp Arg	
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Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys Gln	
370 375 380 385	
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Gly Phe Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile Glu	
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Asn	Glu	Ala	Gly	Ala	Leu	Lys	Leu	Ser	Gly	Leu	Asp	Ala	Ser	Asn	Asp	
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Trp	Gly	Lys	Ser	Val	Asp	Ile	Leu	Gly	Ala	Glu	Lys	Leu	Thr	Met	Asp	
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Val	Ile	Val	Asp	Glu	Pro	Thr	Thr	Val	Ser	Ile	Ala	Ala	Ile	Pro	Gln	
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Gly	Pro	Ser	Ala	Asn	Trp	Val	Asn	Pro	Asn	Arg	Ala	Ile	Lys	Val	Glu	
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cca	act	aat	ttc	gta	ccg	tta	gga	gat	aag	ttt	aaa	gcg	gaa	tta	act	2187
Pro	Thr	Asn	Phe	Val	Pro	Leu	Gly	Asp	Lys	Phe	Lys	Ala	Glu	Leu	Thr	
			485					490					495			
ata	act	tca	gct	gac	tct	cca	tcg	tta	gaa	gct	att	gcg	atg	cat	gct	2235
Ile	Thr	Ser	Ala	Asp	Ser	Pro	Ser	Leu	Glu	Ala	Ile	Ala	Met	His	Ala	
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gaa	aat	aac	aac	atc	aac	aac	atc	att	ctt	ttt	gta	gga	act	gaa	ggt	2283
Glu	Asn	Asn	Asn	Ile	Asn	Asn	Ile	Ile	Leu	Phe	Val	Gly	Thr	Glu	Gly	
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gct	gat	gtt	atc	tat	tta	gat	aac	att	aaa	gta	att	gga	aca	gaa	gtt	2331
Ala	Asp	Val	Ile	Tyr	Leu	Asp	Asn	Ile	Lys	Val	Ile	Gly	Thr	Glu	Val	
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gaa	att	cca	gtt	gtt	cat	gat	cca	aaa	gga	gaa	gct	gtt	ctt	cct	tct	2379
Glu	Ile	Pro	Val	Val	His	Asp	Pro	Lys	Gly	Glu	Ala	Val	Leu	Pro	Ser	
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Val	Phe	Glu	Asp	Gly	Thr	Arg	Gln	Gly	Trp	Asp	Trp	Ala	Gly	Glu	Ser	
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Ala	Thr	Ala	Pro	Arg	Leu	Asp	Phe	Trp	Lys	Ser	Asp	Leu	Val	Arg	Gly	
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Glu	Asn	Asp	Tyr	Val	Thr	Phe	Asp	Phe	Tyr	Leu	Asp	Pro	Val	Arg	Ala	

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645	650	655	
ggg tat tgg gta caa gca cca aaa acg tat acg att aac ttt gat gaa			2715
Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu			
660	665	670	
tta gag gaa gcg aat caa gta aat ggt tta tat cac tat gaa gtg aaa			2763
Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys			
675	680	685	
att aac gta aga gat att aca aac att caa gat gac acg tta cta cgt			2811
Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg			
690	695	700	705
aac atg atg atc att ttt gca gat gta gaa agt gac ttt gca ggg aga			2859
Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg			
710	715	720	
gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct act act gag ccg			2907
Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro			
725	730	735	
gtt gaa cca gag cca gtt gat cct ggc gaa gag acg ccg cct gtc gat			2955
Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp			
740	745	750	
gag aag gaa gcg aaa aaa gaa caa aaa gaa gca gag aaa gaa gag aaa			3003
Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys			
755	760	765	
gaa gca gta aaa gaa gaa aag aaa gaa gct aaa gaa gaa aag aaa gca			3051
Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala			
770	775	780	785
atc aaa aat gag gct acg aaa aaa taatctaata aactagttat agggttatct			3105
Ile Lys Asn Glu Ala Thr Lys Lys			
790			
aaagggtctga tgcagatctt ttagataacc tttttttgca taactggaca tagaatgggt			3165
attaaagaaa gcaagggtgtt tatacgatat taaaaaggta gcgatttttaa attgaaacct			3225
ttaataatgt cttgtgatag aatgatgaag taatttaaga gggggaaacg aagtgaaaac			3285
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Glu	Gly	Trp	Asn	Ala	Val	Lys	Glu	Tyr	Ala	Asp	Pro	Ile	Val	Glu	Met	
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Leu	Arg	Asp	Ser	Gly	Asn	Ala	Asp	Asp	Asn	Ile	Ile	Ile	Val	Gly	Ser	
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Pro	Asn	Trp	Ser	Gln	Arg	Pro	Asp	Leu	Ala	Ala	Asp	Asn	Pro	Ile	Asp	
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Asp His His Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala
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Ala Ser Thr Glu Ser Tyr Pro Pro Glu Thr Pro Asn Ser Glu Arg Gly
 245 250 255

Asn Val Met Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val
 260 265 270

Phe Ala Thr Glu Trp Gly Thr Ser Gln Ala Asn Gly Asp Gly Gly Pro
 275 280 285

Tyr Phe Asp Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn
 290 295 300

Ile Ser Trp Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly
 305 310 315 320

Ala Phe Thr Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Ser Leu Asp
 325 330 335

Pro Gly Pro Asp Gln Val Trp Val Pro Glu Glu Leu Ser Leu Ser Gly
 340 345 350

Glu Tyr Val Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp
 355 360 365

Arg Thr Lys Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys
 370 375 380

Gln Gly Phe Gly Val Asn Gly Asp Ser Pro Val Glu Asp Val Val Ile
 385 390 395 400

Glu Asn Glu Ala Gly Ala Leu Lys Leu Ser Gly Leu Asp Ala Ser Asn
 405 410 415

Asp Val Ser Glu Gly Asn Tyr Trp Ala Asn Ala Arg Leu Ser Ala Asp
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Gly Trp Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met
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Asp Val Ile Val Asp Glu Pro Thr Thr Val Ser Ile Ala Ala Ile Pro

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Gln Gly Pro Ser Ala Asn Trp Val Asn Pro Asn Arg Ala Ile Lys Val				
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Glu Pro Thr Asn Phe Val Pro Leu Gly Asp Lys Phe Lys Ala Glu Leu				
		485		490
				495
Thr Ile Thr Ser Ala Asp Ser Pro Ser Leu Glu Ala Ile Ala Met His				
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Ala Glu Asn Asn Asn Ile Asn Asn Ile Ile Leu Phe Val Gly Thr Glu				
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Gly Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu				
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Val Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro				
545		550		555
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Ser Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu				
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Ser Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn				
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Ala Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn				
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Trp Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg				
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				620
Gly Glu Asn Asp Tyr Val Thr Phe Asp Phe Tyr Leu Asp Pro Val Arg				
625		630		635
				640
Ala Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr				
		645		650
				655
Asn Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp				
		660		665
				670
Glu Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val				
		675		680
				685

Lys Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu
690 695 700

Arg Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly
705 710 715 720

Arg Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu
725 730 735

Pro Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val
740 745 750

Asp Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu
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gaaataaaaag tagaagacaa aggacataag aaaattgcat tagttttaat tatagaaaac 180
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gtaagcgggtt aaccttggtc tatatgccga tttaggaagg ggggtagaat atttcaagta 420
gtaataacat acaataactta taagttgttg agaagcagga gagcatctgg gttactcaca 480
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 cctgattttta ttttttttgaa ttttttttgag aactaaagat tgaaatagaa gtagaagaca 180
 acggacataa gaaaattgta ttagttttta ttatagaaaa cgcttttcta taattattta 240
 tacctagaac gaaaatactg tttcgaaagc ggtttactat aaaaccttat attccggctc 300
 ttttttttaaa caggggggtga aaattcactc tagtattcta atttcaacat gctataataa 360
 atttgtaaga cgcaatatac atcttttttt tatgatattt gtaagcgggt aaccttgtgc 420
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 aagttgttga gaagcaggag agaatctggg ttactcacia gtttttttaa acattatcga 540
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<220>
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<400> 9
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<210> 10
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 <213> artificial sequence

<220>
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<210> 11
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      f Bacillus sp. KSM-S237 gene for cellulase; the sequence containi
      ng eight nucleotides substitution for SigmaE recognition

<400> 11
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<210> 12
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aatgacatc atataaacia atttgtctac caatcactat tttaaagctgt ttatgatata      180

tgtaagcggt atcattaaaa ggaggtatgt g atg aga aga tgg gta gta gca      232
                        Met Arg Arg Trp Val Val Ala
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atg ttg gca gtg tta ttt tta ttt cct tcg gta gta gtt gca gat gga	280
Met Leu Ala Val Leu Phe Leu Phe Pro Ser Val Val Val Ala Asp Gly	
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Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu Asn Asp	
5 10 15	
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Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu Ser Asp	
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gct ggt att aca gct att tgg att ccg cca gcc tac aaa ggt aat agt	424
Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly Asn Ser	
35 40 45 50	
cag gcg gat gtt ggg tac ggt gca tac gat ctt tat gat tta gga gag	472
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu	
55 60 65	
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Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ala Gln	
70 75 80	
ctt gaa cga gct att ggg tcc ctt aaa tct aat gat atc aat gta tac	568
Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn Val Tyr	
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Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr Glu Ala	
100 105 110	
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Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp Ile Ser	
115 120 125 130	
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Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser Gly Arg	
135 140 145	
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Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe Asn Gly	
150 155 160	
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Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg Phe Ala	
165 170 175	
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Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val Gln Asp	
195 200 205 210	

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gat tgg gtt cgg cat cag cgc aac gaa gca gat caa gat tta ttt gtc Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu Phe Val 245 250 255	1048
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aac gat aac att tca gct aaa aaa gat atg att gat gag ctg ctt gat Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu Leu Asp 375 380 385	1432
gca cgt caa aat tac gca tat ggc acg cag cat gac tat ttt gat cat Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe Asp His 390 395 400	1480
tgg gat gtt gta gga tgg act agg gaa gga tct tcc tcc aga cct aat Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Arg Pro Asn 405 410 415	1528
tca ggc ctt gcg act att atg tcg aat gga cct ggt ggt tcc aag tgg Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser Lys Trp 420 425 430	1576
atg tat gta gga cgt cag aat gca gga caa aca tgg aca gat tta act	1624

Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp Leu Thr
435 440 445 450

ggt aat aac gga gcg tcc gtt aca att aat ggc gat gga tgg ggc gaa 1672
Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp Gly Glu
455 460 465

ttc ttt acg aat gga gga tct gta tcc gtg tac gtg aac caa taacaaaaa 1723
Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
470 475 480

gccttgagaa gggattcctc cctaactcaa ggctttcttt atgtcgctta gctttacgct 1783

tctacgactt tg 1795

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<212> PRT
<213> Bacillus sp. KSM-K38

<400> 14

Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu
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Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu
20 25 30

Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
85 90 95

Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr
100 105 110

Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp
115 120 125

Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser
130 135 140

Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
 145 150 155 160

Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg
 165 170 175

Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
 180 185 190

Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
 195 200 205

Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
 210 215 220

Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
 225 230 235 240

Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu
 245 250 255

Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
 260 265 270

Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
 275 280 285

Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met
 290 295 300

Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
 305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
 325 330 335

Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
 340 345 350

Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
 355 360 365

Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
 370 375 380

Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
 385 390 395 400

Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg
 405 410 415

Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
 420 425 430

Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
 435 440 445

Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
 450 455 460

Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
 465 470 475 480

<210> 15
 <211> 25
 <212> DNA
 <213> artificial sequence

<220>
 <223> Oligonucleotide as PCR primer designed from nucleotide sequence of Bacillus sp. KSM-S237 gene for cellulase; the sequence with a insertion of the BamHI restriction site at the 5'-end

<400> 15
 cccggtacca acaggcttat atttta 25

<210> 16
 <211> 29
 <212> DNA
 <213> artificial sequence

<220>
 <223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of Bacillus sp. KSM-S237 gene for cellulase and its 5'-portion designed from nucleotide sequence of Bacillus sp. KSM-K38 gene for amylase

<400> 16
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<210> 17
 <211> 30
 <212> DNA
 <213> artificial sequence

 <220>
 <223> Oligonucleotide as PCR primer; its 3'-portion designed from nucleotide sequence of Bacillus sp. KSM-K38 gene for amylase and its 5'-portion designed from nucleotide sequence of Bacillus sp. KSM-S237 gene for cellulase

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 gctcttgcag cagatggatt gaacggtacg 30

 <210> 18
 <211> 30
 <212> DNA
 <213> artificial sequence

 <220>
 <223> Oligonucleotide as PCR primer designed from nucleotide sequence of Bacillus sp. KSM-K38 gene for amylase; the sequence with a insertion of the XbaI restriction site at the 5'-end

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